SEQUENCE LISTING

<110> Pharmacia AB

<120> Protein Cluster II

<130> 00404

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<170> PatentIn version 3.0

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<223> n=a, g, c or t

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                       Met Thr Glu Asn Ser Leu Ser Glu Met Ala Ser
                       1               5                  10

aaa tcc tgg ctg aat ttt tta acc ttc ctc tat gga tcg gca ata ggg      101
Lys Ser Trp Leu Asn Phe Leu Thr Phe Leu Tyr Gly Ser Ala Ile Gly
            15                  20                  25

ttt att tta ttt tct cag cta ctt agt att ttg ttg gga gaa gag ggt      149
Phe Ile Leu Phe Ser Gln Leu Leu Ser Ile Leu Leu Gly Glu Glu Gly
        30                  35                  40

gac acc cag act aat gtt ctt cat aat gat cct cat gcg agg cat tca      197
Asp Thr Gln Thr Asn Val Leu His Asn Asp Pro His Ala Arg His Ser
    45                  50                  55

gat gat aat gga cag aat cat cta gga gga caa atg aac ttc aat gca      245
Asp Asp Asn Gly Gln Asn His Leu Gly Gly Gln Met Asn Phe Asn Ala
60                  65                  70                  75

gat tct agc caa cgt aaa gat gag aac aca gaa atc gct gaa aac ctc      293
Asp Ser Ser Gln Arg Lys Asp Glu Asn Thr Glu Ile Ala Glu Asn Leu
                80                  85                  90

tat nag caa gtt aaa att ctt tgc tgg gtt atg aca ggc tct caa aac      341
Tyr Xaa Gln Val Lys Ile Leu Cys Trp Val Met Thr Gly Ser Gln Asn
            95                  100                 105

cta cag aaa aag gcc aaa cat gtc aaa gct aca tgg gcc cag cgt tgt      389
Leu Gln Lys Lys Ala Lys His Val Lys Ala Thr Trp Ala Gln Arg Cys
        110                 115                 120

cta aaa gta ttt ttt atg agt tca gaa gaa aat aaa gac ttc cgt gct      437
Leu Lys Val Phe Phe Met Ser Ser Glu Glu Asn Lys Asp Phe Arg Ala
    125                 130                 135

gtg gga ttg aaa acc aaa gca ggc aga gat gag cta tac tgg aaa aca      485
Val Gly Leu Lys Thr Lys Ala Gly Arg Asp Glu Leu Tyr Trp Lys Thr
140                 145                 150                 155

att aac ctt ttc agtatgtt                                            505
Ile Asn Leu Phe
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Phe Leu Thr Phe Leu Tyr Gly Ser Ala Ile Gly Phe Ile Leu Phe Ser
20 25 30

Gln Leu Leu Ser Ile Leu Leu Gly Glu Glu Gly Asp Thr Gln Thr Asn
35 40 45

Val Leu His Asn Asp Pro His Ala Arg His Ser Asp Asp Asn Gly Gln
50 55 60

Asn His Leu Gly Gly Gln Met Asn Phe Asn Ala Asp Ser Ser Gln Arg
65 70 75 80

Lys Asp Glu Asn Thr Glu Ile Ala Glu Asn Leu Tyr Xaa Gln Val Lys
85 90 95

Ile Leu Cys Trp Val Met Thr Gly Ser Gln Asn Leu Gln Lys Lys Ala
100 105 110

Lys His Val Lys Ala Thr Trp Ala Gln Arg Cys Leu Lys Val Phe Phe
115 120 125

Met Ser Ser Glu Glu Asn Lys Asp Phe Arg Ala Val Gly Leu Lys Thr
130 135 140

Lys Ala Gly Arg Asp Glu Leu Tyr Trp Lys Thr Ile Asn Leu Phe
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aca ggt gtc act gac aaa ctc tat caa aag atg aaa att ctt tgc tgg 105

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Thr Gly Val Thr Asp Lys Leu Tyr Gln Lys Met Lys Ile Leu Cys Trp
          5                  10                  15

att atg aca gga cct caa aat cta gaa aaa aag atc aga cgc atc aga      153
Ile Met Thr Gly Pro Gln Asn Leu Glu Lys Lys Ile Arg Arg Ile Arg
        20                  25                  30

gat aca tgg gcc cag ggt tgc aat aaa gcg ttg ttt atg agc tca aaa      201
Asp Thr Trp Ala Gln Gly Cys Asn Lys Ala Leu Phe Met Ser Ser Lys
    35                  40                  45

gaa aat aaa gac ttc tct act gtg gga tta cac acc aaa gaa gac aga      249
Glu Asn Lys Asp Phe Ser Thr Val Gly Leu His Thr Lys Glu Asp Arg
50                  55                  60                  65

aac caa ctg tcc tgg aaa ata gtt aaa gct ttt cta tat gct cat gac      297
Asn Gln Leu Ser Trp Lys Ile Val Lys Ala Phe Leu Tyr Ala His Asp
                70                  75                  80

cat tat ctg gaa tac atg gat tgg ttc atg aaa gca gat gat gat ata      345
His Tyr Leu Glu Tyr Met Asp Trp Phe Met Lys Ala Asp Asp Asp Ile
            85                  90                  95

tgt ata tat atc aca ttg gac aac ttg aaa tgg ctt ctc aca aac tat      393
Cys Ile Tyr Ile Thr Leu Asp Asn Leu Lys Trp Leu Leu Thr Asn Tyr
        100                 105                 110

aac cct gat gaa tcc act tac ttt ggg aaa aga ttt aag cac tgc aga      441
Asn Pro Asp Glu Ser Thr Tyr Phe Gly Lys Arg Phe Lys His Cys Arg
    115                 120                 125

aaa cag gac tac atg act gga gga gca gga tat gta ctg agc aaa gaa      489
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130                 135                 140                 145
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Trp Ile Met Thr Gly Pro Gln Asn Leu Glu Lys Lys Ile Arg Arg Ile
            20                  25                  30

Arg Asp Thr Trp Ala Gln Gly Cys Asn Lys Ala Leu Phe Met Ser Ser
        35                  40                  45

Lys Glu Asn Lys Asp Phe Ser Thr Val Gly Leu His Thr Lys Glu Asp
    50                  55                  60

Arg Asn Gln Leu Ser Trp Lys Ile Val Lys Ala Phe Leu Tyr Ala His
65                  70                  75                  80

Asp His Tyr Leu Glu Tyr Met Asp Trp Phe Met Lys Ala Asp Asp Asp
                85                  90                  95

Ile Cys Ile Tyr Ile Thr Leu Asp Asn Leu Lys Trp Leu Leu Thr Asn
            100                 105                 110
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Tyr Asn Pro Asp Glu Ser Thr Tyr Phe Gly Lys Arg Phe Lys His Cys
        115                 120                 125

Arg Lys Gln Asp Tyr Met Thr Gly Gly Ala Gly Tyr Val Leu Ser Lys
    130                 135                 140

Glu
145
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Sub B1

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  1               5                  10                  15

tct agc caa cat aaa gat gag aac aca gac att gct gaa aac ctc tat      97
Ser Ser Gln His Lys Asp Glu Asn Thr Asp Ile Ala Glu Asn Leu Tyr
            20                  25                  30

cag aaa gtt aga att ctt tgc tgg gtt atg acc ggc cct caa aac cta     145
Gln Lys Val Arg Ile Leu Cys Trp Val Met Thr Gly Pro Gln Asn Leu
        35                  40                  45

gag aaa aag gcc aaa cac gtc aaa gct act tgg gcc cag cgt tgt aac     193
Glu Lys Lys Ala Lys His Val Lys Ala Thr Trp Ala Gln Arg Cys Asn
    50                  55                  60

aaa gtg ttg ttt atg agt tca gaa gaa aat aaa gac ttc cct gct gtg     241
Lys Val Leu Phe Met Ser Ser Glu Glu Asn Lys Asp Phe Pro Ala Val
65                  70                  75                  80

gga ctg aaa acc aaa gaa ggc aga gat caa cta tac tgg aaa aca att     289
Gly Leu Lys Thr Lys Glu Gly Arg Asp Gln Leu Tyr Trp Lys Thr Ile
                85                  90                  95

aaa gct ttt cag tat gtt cat gaa cat tat tta caa gat gct gat tgg     337
Lys Ala Phe Gln Tyr Val His Glu His Tyr Leu Gln Asp Ala Asp Trp
            100                 105                 110

ttt ttg aaa gca gat gat gac acg tat gtc ata cta gac aat ttg agg     385
Phe Leu Lys Ala Asp Asp Asp Thr Tyr Val Ile Leu Asp Asn Leu Arg
        115                 120                 125

tgg ctt ctt tca aaa tac gac cct gaa gaa ccc att tac ttt ggg aga     433
Trp Leu Leu Ser Lys Tyr Asp Pro Glu Glu Pro Ile Tyr Phe Gly Arg
    130                 135                 140

aga ttt aag cct tat gta aag cag ggc tac atg agt gga gga gca gga     481
Arg Phe Lys Pro Tyr Val Lys Gln Gly Tyr Met Ser Gly Gly Ala Gly
145                 150                 155                 160

tat gta cta agc aaa gaa gcc ttg aaa aga ttt gtt gat gca ttt aaa     529
Tyr Val Leu Ser Lys Glu Ala Leu Lys Arg Phe Val Asp Ala Phe Lys
                165                 170                 175

aca gac aag tgt aca cat agt tcc tcc att gaa gac tta gca ctg ggg     577
Thr Asp Lys Cys Thr His Ser Ser Ser Ile Glu Asp Leu Ala Leu Gly
            180                 185                 190
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aga tgc atg gaa att atg aat gta gaa gca gga gat tcc aga gat acc      625
Arg Cys Met Glu Ile Met Asn Val Glu Ala Gly Asp Ser Arg Asp Thr
        195                 200                 205

att gga aaa gaa act ttt cat ccc ttt gtg cca gaa cac cat tta att      673
Ile Gly Lys Glu Thr Phe His Pro Phe Val Pro Glu His His Leu Ile
    210                 215                 220

aaa ggt tat cta cct aga acg ttt tgg tac tgg aat tac aac tat tat      721
Lys Gly Tyr Leu Pro Arg Thr Phe Trp Tyr Trp Asn Tyr Asn Tyr Tyr
225                 230                 235                 240

cct cct gta gag ggt cct ggt tgc tgc tct gat ctt gca gtt tct ttt      769
Pro Pro Val Glu Gly Pro Gly Cys Cys Ser Asp Leu Ala Val Ser Phe
                245                 250                 255

cac tat gtt gat tct aca acc atg tat gag tta gaa tac ctc gtt tat      817
His Tyr Val Asp Ser Thr Thr Met Tyr Glu Leu Glu Tyr Leu Val Tyr
            260                 265                 270

cat ctt cgt cca tat ggt tat tta tac aga tat caa cct acc tta cct      865
His Leu Arg Pro Tyr Gly Tyr Leu Tyr Arg Tyr Gln Pro Thr Leu Pro
        275                 280                 285

gaa cgt ata cta aag gaa att agt caa gca aac aaa aat gaa gat aca      913
Glu Arg Ile Leu Lys Glu Ile Ser Gln Ala Asn Lys Asn Glu Asp Thr
    290                 295                 300

aaa gtg aag tta gga aat cct tgaaagaaaa tcatgaatga acaaaggtaa        964
Lys Val Lys Leu Gly Asn Pro
305                 310

tatgtctagc actgcactga aaaaggactt ctgcatttct gacatagaac actggaatcc   1024

cagtgaggaa ttctaagtga acattcctta tagaaacctt tcacatgaat gactataaac   1084

tgaagcttta aatgagctgt gaagtgtgtt aaaatgtgtt ttgatacagt aatatataaa   1144

tatgtctata tatatgagga acttgtgttt tttaaatggt ggccaggtag aggaactaga   1204

aaagagattt tgttgcctgt tttctgacca tctgtgttat tgtcactgag aaactaaaat   1264

agtaaattta ctaaaactac actgcaccat gttagtaata aacagatctg ccttaaagaa   1324

aagaaaattt tagaaagaaa tattgttgct cagtgttgtt aatatagctc aagaattgag   1384

tttatatttg cagtatgcta taaatgatac ccccctacca cacccacaca cacagttttt   1444

gtctaatgaa aatgttgctg tgattattta taattggtag tatttcttcc agaagaagct   1504

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            20                  25                  30

Gln Lys Val Arg Ile Leu Cys Trp Val Met Thr Gly Pro Gln Asn Leu
        35                  40                  45
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Glu Lys Lys Ala Lys His Val Lys Ala Thr Trp Ala Gln Arg Cys Asn
50 55 60

Lys Val Leu Phe Met Ser Ser Glu Glu Asn Lys Asp Phe Pro Ala Val
65 70 75 80

Gly Leu Lys Thr Lys Glu Gly Arg Asp Gln Leu Tyr Trp Lys Thr Ile
85 90 95

Lys Ala Phe Gln Tyr Val His Glu His Tyr Leu Gln Asp Ala Asp Trp
100 105 110

Phe Leu Lys Ala Asp Asp Asp Thr Tyr Val Ile Leu Asp Asn Leu Arg
115 120 125

Trp Leu Leu Ser Lys Tyr Asp Pro Glu Glu Pro Ile Tyr Phe Gly Arg
130 135 140

Arg Phe Lys Pro Tyr Val Lys Gln Gly Tyr Met Ser Gly Gly Ala Gly
145 150 155 160

Tyr Val Leu Ser Lys Glu Ala Leu Lys Arg Phe Val Asp Ala Phe Lys
165 170 175

Thr Asp Lys Cys Thr His Ser Ser Ser Ile Glu Asp Leu Ala Leu Gly
180 185 190

Arg Cys Met Glu Ile Met Asn Val Glu Ala Gly Asp Ser Arg Asp Thr
195 200 205

Ile Gly Lys Glu Thr Phe His Pro Phe Val Pro Glu His His Leu Ile
210 215 220

Lys Gly Tyr Leu Pro Arg Thr Phe Trp Tyr Trp Asn Tyr Asn Tyr Tyr
225 230 235 240

Pro Pro Val Glu Gly Pro Gly Cys Cys Ser Asp Leu Ala Val Ser Phe
245 250 255

His Tyr Val Asp Ser Thr Thr Met Tyr Glu Leu Glu Tyr Leu Val Tyr
260 265 270

His Leu Arg Pro Tyr Gly Tyr Leu Tyr Arg Tyr Gln Pro Thr Leu Pro
275 280 285

Glu Arg Ile Leu Lys Glu Ile Ser Gln Ala Asn Lys Asn Glu Asp Thr
290 295 300

Lys Val Lys Leu Gly Asn Pro
305 310